

Title: Understanding the genetic diversity in order to identify *R*-genes in *Oryza* spp. and *O. sativa*

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Rice wild relatives (*Oryza* spp.) and introduced rice (*O. sativa*) germplasm are important sources of novel *R*(resistance)-genes for rice improvement. Rice sheath blight, caused by *Rhizotonia solani*, and leaf blast, caused by *Magnaportha grisea*, are major fungal diseases of irrigated rice worldwide. In order to identify novel resistance genes, one group of *Oryza* spp. accessions represented by *O. alta*, *O. australiensis*, *O. barthii*, *O. glaberrima*, *O. glumapatula*, *O. latifolia*, *O. meridionolis*, *O. nivara*, *O. officinalis*, and *O. rufipogon*, and a second group of *O. sativa* accessions, many of which were identified as blast resistant in the field, were tested for resistance to U.S. blast races in the greenhouse and sheath blight resistance. A third group of U.S. cultivars was included for comparison. The accessions were genotyped with approximately 200 SSR markers, including markers associated with blast resistance (*Pi*-) genes and data from the SSR markers used to conduct genetic distance and cluster analysis. Marker-trait associations between the aforementioned SSR markers and the disease reactions to blast races and sheath blight were delineated using the PowerMarker software. Associations identified with SSR markers were compared between the two groups and to the locations of known blast resistance genes and sheath blight QTL. Mapping populations are being developed from blast resistant accessions for fine mapping and identification of novel *R*-genes. Selected germplasm will be made available to rice breeding programs.